Bioinformatics
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TOBMI: trans-omics block missing data imputation using a k-nearest neighbor weighted approach
J.Deng, L.Li, K.Zhang, Y.Zhou, D.C.Christiansen, Y.Wei and F.Chen

Combining count- and length-based z-scores leads to improved predictions in non-invasive prenatal testing

Inference and visualization of DNA damage patterns using a grade of membership model
H.AI-Asadi, K.Dey, J.Novembre and M.Stephens

smCounter2: an accurate low-frequency variant caller for targeted sequencing data with unique molecular identifiers

Dante: genotyping of known complex and expanded short tandem repeats
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A Bayesian framework for high-throughput T cell receptor pairing
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RNApuzzler: efficient outerplanar drawing of RNA-secondary structures
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Genetics and population analysis
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A clustering linear combination approach to jointly analyze multiple phenotypes for GWAS
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Filtering and inference for stochastic oscillators with distributed delays
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